REMARKS

In addition to the restricting the claims, the immunodeficiency virus type, the deletion region, and the nucleic acid sequence, the Examiner further alleges that, with respect to the amino acid mutations encompassed by claims 7-11 in Group I, yet an additional election of a *single* mutation must be made in response to the restriction requirement. Applicants respectfully traverse the mutation election set forth by the Examiner.

Applicants, in a good faith effort to expedite the prosecution of this application, hereby provisionally elect to prosecute the claims of Group I. Applicants also elect: 1) human immunodeficiency virus type 2 (HIV-2); 2) deletion of V3 region (ΔV3(6,6)); and 3) the sequence of "SEQ ID NO:11" within Group I claims. Further, Applicants *provisionally* elect the mutation of amino acid position number 393, with respect to claims 7-11. Nonetheless, Applicants traverse the Examiner's sequence restriction with respect to the election of a single mutation within the amino acid mutations encompassed by claims 7-11, as more fully set forth below.

Under the "Guidelines" for restriction requirement practice, the Examiner is required to "provide reasons and/or examples to support conclusions" for the restriction requirement in view of the standard set forth in MPEP 803. However, in the present action, the Examiner has not provided any reason or rationale regarding the imposition of the "mutation restriction." In particular, the Examiner has not provided any explanation pertaining to the notion that searching all of the mutants encompassed by claims 7-11 of Group I would impose a serious search burden, or that such a search and analysis of the search results would be complex in nature. In fact, in view of the multiple restrictions imposed by the Examiner, the mutation search would be even less burdensome than it was prior to the Examiner's restrictions.

Applicants traverse the present mutation restriction requirement because Applicants respectfully contend that in the event that the Examiner performs a prior art search directed to SEQ ID NO:11, for example, the Examiner will necessarily uncover art pertaining to one of the finite number of amino acid mutants of SEQ ID NO:11 as set forth in claim 7, for example, if such art exists. This is because any mutant as set forth in claims 7-11 is necessarily encompassed by elected SEQ ID NO:11. That is, each of said mutants is included within the elected SEQ ID NO:11, if such a mutant of SEQ ID NO:11 is made according to the invention.

Even if SEQ ID NO:11 according to the elected invention were to contain all of the mutations set forth in claim 7, for example, the total number of claimed mutations is only a fractional percentage of the total number of amino acid residues in SEQ ID NO:11. As Applicants understand the manner and methods used to search polypeptide sequence databases, and as the Examiner should similarly be aware, a search of the relevant databases for a mutant SEQ ID NO:11 will necessarily turn up SEQ ID NO:11, and vice versa, if such art indeed exists.

Applicants hereby state that no comparison or statement is being made herein regarding novelty or patentability of SEQ ID NO:11 in view of any mutant of SEQ ID NO:11, or vice versa. Rather, Applicants' instant traversal pertains solely to the search burden imposed upon the Examiner.

Accordingly, Applicants respectfully request withdrawal of the mutation restriction.

Summary

Applicants respectfully request withdrawal of the mutation restriction requirement. In doing so, Applicants make no assertion as to the relatedness of the sequences or claims restricted by the Examiner. Rather, Applicants merely respond herein to the Examiner's invitation, and respectfully submit that the Examiner has not met her burden in demonstrating that a prior art search of all mutations in the pending claims would be unduly burdensome.

Withdrawal of the mutation restriction and examination of all pending claims on the merits at the earliest possible time is respectfully requested.

Respectfully submitted,

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